WO 2005/076008 PCT/EP2005/000722

-1-

SEQUENCE LISTING

<110> Bayer HealthCare AG

<120> Diagnostics and Therapeutics for Diseases Associated with Phosphate Regulating Endopeptidase Homolog (PHEX)

<130> BHC 04 01 031

<160> 5

<170> PatentIn version 3.2

<210> 1

<211> 2590

<212> DNA

<213> Homo sapiens

<400> 1

aacgcctcgc tcttgagacc agccaccaaa ccacgaaaag tgactttctt ctcgtgtgct 60 ctctacggcc cttctgatgg aagcagaaac agggagcagc gtggagactg gaaagaaggc 120 caacagaggc actcgaattg ccctggtcgt gtttgtcggt ggcaccctag ttctgggcac 180 gatectettt etagtgagte aaggtetett aagteteeaa getaaacagg agtactgeet 240 gaagccagaa tgcatcgaag cggctgctgc catcttaagt aaagtaaatc tgtctgtgga 300 tccttgtgat aatttcttcc ggttcgcttg tgatggctgg ataagcaata atccaattcc 360 cgaagatatg ccaagctatg gggtttatcc ttggctgaga cataatgttg acctcaagtt 420 gaaggaactt ttggagaaat caatcagtag aaggcgggac accgaagcca tacagaaagc 480 caaaatcctt tattcatcct gcatgaatga gaaagcgatt gaaaaagcag atgccaagcc 540 actgctacac atcctacggc attcaccttt ccgctggccc gtgcttgaat ctaatattgg 600 ccctgaaggg gtttggtcag agagaaagtt cagccttctg cagacacttg caacgtttcg 660 tggtcaatac agcaattctg tgttcatccg tttgtatgtg tcccctgatg acaaagcatc 720 caatgaacat atcttgaagc tggaccaagc aacactctcc ctggccgtga gggaagacta 780 ccttgataac agtacagaag ccaagtctta tcgggatgcc ctttacaagt tcatggtgga 840 900 cagattggaa attaagatag ctgagataat gattccacat gaaaaccgaa ccagcgaggc 960 catgtacaac aaaatgaaca tttctgaact gagtgctatg attccccagt tcgactggct 1020 gggctacatc aagaaggtca ttgacaccag actctacccc catctgaaag acatcagccc 1080 ctccgagaat gtggtggtcc gcgtcccgca gtactttaaa gatttgttta ggatattagg 1140 gtctgagaga aagaagacca ttgccaacta tttggtgtgg agaatggttt attccagaat 1200 tccaaacctt agcaggcgct ttcagtatag atggctggaa ttctcaaggg taatccaggg 1260 gaccacaact ttgctgcctc aatgggacaa atgtgtaaac tttattgaaa gtgccctccc 1320 ttatgttgtt ggaaagatgt ttgtagatgt gtacttccag gaagataaga aggaaatgat 1380 ggaggaattg gttgagggcg ttcgctgggc ctttattgac atgctagaga aagaaatga 1440 gtggatggat gcaggaacga aaaggaaagc caaagaaaag gcgagagctg ttttggcaaa 1500 agttggctat ccagagttta taatgaatga tactcatgtt aatgaagacc tcaaaqctat 1560

-2caagttttca gaagccgact actttggcaa cgtcctacaa actcgcaagt atttagcaca 1620
gtctgatttc ttctggctaa gaaaagccgt tccaaaaaca gagtggttta caaatccgac 1680
gactgtcaat gccttctaca gtgcatccac caaccagatc cgatttccag caggagagct 1740

PCT/EP2005/000722

ccagaagcct ttcttttggg gaacagaata tcctcgatct ctgagttatg gtgctatagg 1800 agtaattgtc ggacatgaat ttacacatgg atttgataat aatggtagaa aatatgataa 1860 aaatggaaac ctggatcctt ggtggtctac tgaatcagaa gaaaagttta aggaaaaaac 1920 aaaatgcatg attaaccagt atagcaacta ttattggaag aaagctggct taaatgtcaa 1980 ggggaagagg accctgggag aaaatattgc tgataatgga ggcctgcggg aagcttttag 2040 ggcttacagg aaatggataa atgacagaag gcagggactt gaggagcctc ttctaccagg 2100 catcacattc accaacaacc agetettett cetgagttat geteatgtga ggtgcaatte 2160 ctacagacca gaagctgccc gagaacaagt ccaaattggt gctcacagtc cccctcagtt 2220 tagggtcaat ggtgcaatta gtaactttga agaattccag aaagctttta actgtccacc 2280 caattccacg atgaacagag gcatggactc ctgccgactc tggtagctgg gacgctggtt 2340 tatggcatcc tgagacagtt gcacagtgcc agcggaggct gcactgagcc ttcatcgccc 2400 attgctttag gcctggagac tttcattttt agtgcatttt cattatttgg gtaggtgacc 2460 tgcttggatc tagacagcat ctgttcaaag tcgtagggct tataaagtgg aatataagaa 2520 tgaactaagt atgtttcttt agaaaatcaa accaacaaaa ataaatccct aggctacttt 2580 tgttaaaaaa 2590

<210> 2

WO 2005/076008

<211> 749

<212> PRT

<213> Homo sapiens

<400> 2

145

Met Glu Ala Glu Thr Gly Ser Ser Val Glu Thr Gly Lys Lys Ala Asn Arg Gly Thr Arg Ile Ala Leu Val Val Phe Val Gly Gly Thr Leu Val Leu Gly Thr Ile Leu Phe Leu Val Ser Gln Gly Leu Leu Ser Leu Gln 40 Ala Lys Gln Glu Tyr Cys Leu Lys Pro Glu Cys Ile Glu Ala Ala Ala 55 Ala Ile Leu Ser Lys Val Asn Leu Ser Val Asp Pro Cys Asp Asn Phe 75 80 Phe Arg Phe Ala Cys Asp Gly Trp Ile Ser Asn Asn Pro Ile Pro Glu 90 Asp Met Pro Ser Tyr Gly Val Tyr Pro Trp Leu Arg His Asn Val Asp 105 110 Leu Lys Leu Lys Glu Leu Leu Glu Lys Ser Ile Ser Arg Arg Arg Asp 120 Thr Glu Ala Ile Gln Lys Ala Lys Ile Leu Tyr Ser Ser Cys Met Asn

Glu Lys Ala Ile Glu Lys Ala Asp Ala Lys Pro Leu Leu His Ile Leu

155

160

150

- 3 -

Arg	His	s Ser	Pro	Phe 165	-	Trp	Pro	Val	Leu 170		Ser	Asn	ılle	Gly	Pro
Gla	G Lu	r Val	Trr			Ara	Tars	Phe			T.e.1	GI n	Thr		Ala
020	. 017	742	180		010	9	Lys	185	Del	200	шеа	GIII	190		. Ala
Thr	Phe	Arg	gly	Gln	Tyr	Ser	Asn	Ser	Val	Phe	Ile	Arg	Leu	Tyr	Val
		195	5		_		200					205		-	
Ser	Pro	Asp	Asp	Lys	Ala	Ser	Asn	Glu	His	Ile	Leu	Lys	Leu	Asp	Gln
	210		_	_		215					220	•		-	
Ala	Thr	Leu	Ser	Leu	Ala	Val	Arq	Glu	Asp	Tvr		Asp	Asn	Ser	Thr
225					230		J		_	235					240
_		Lvs	Ser	Tvr		Asp	Ala	Leu	Tyr		Phe	Met	Val	Asp	
		•		245	_				250					255	
Ala	Val	Len	Tien			Agn	Ser	Ser	Arg	Δla	G 111	Hie	Δen		
			260	_				265					270		-7-2
Ser	Val	Ten			G] 11	Tle	Tve		Ala	Glu	Tle	Met		Pro	Иie
		275					280		mu			285		1	1113
Glar	Agn			Ser	G] 11	Δla		TTSETT	Asn	Tare	Met-		Tla	Ser	GI 11
	290			501	014	295	ن بدر	-7-	HOIL	11 2 2	300	*****		Der	0
T.011		7A 7 ==	Mot	TIA	Pro		Pho	7) ero	Trp	T.OTT		Terro	TIO	Tara	Larg
305	per	Ala	Mer	TT6	310	G1.11	FIIG	Asp	ırp	315	GTĀ	туг	TTG	пуѕ	дуs 320
	TIO	7.55	mb m	7		M====	Desc	TT-1	T		3	~ 7 ~	C	D===	
val	TTE	ASD	TIIT			IAT	PLO	HIS	Leu	цуs	Asp	TTG	ser		Ser
a 1	7	77- 7	77- 7	325		TT_ 7	D	a 7	330	5 1	-	3	.	335	3
GIU	ASII	var		vaı	Arg	vaı	PTO		Tyr	Pne	ьys	Asp		Pne	Arg
T7 -	T	~7	340	~ 1		-		345					350	4	
тте	ьеп	_	ser	GIU	arg	гÀг	_	Thr	Ile	Ата	Asn	-	геп	val	rrp
3	35-4-	355		a			360		_	_	_	365	1		_
Arg		vaı	Tyr	ser	Arg		Pro	Asn	Leu	ser	_	Arg	Pne	GTU	Tyr
•	370	_	~-			375					380			_	_
	Trp	ьеи	GIU	Pne		Arg	vaı	тте	Gln		Thr	unr	Thr	ьеп	
385		_	_	_	390	=	_			395	_		_	_	400
Pro	GIN	Trp	Asp		Cys	Val	Asn	Phe	Ile	GLu	Ser	Ala	Leu		Tyr
			_	405		-	_		410					415	_
Val	Val	GTA		Met	Phe	Val	Asp		Tyr	Phe	Gln	GLu		Lys	Lys
			420			_		425		_	_		430		_
Glu	Met		Glu	Glu	Leu	Val		Gly	Val	Arg	Trp		Phe	Ile	Asp
		435					440					445			
Met		Glu	Lys	Glu	Asn		Trp	Met	Asp	Ala	_	Thr	Lys	Arg	Lys
	450					455					460				
Ala	Lys	Glu	Lys	Ala	Arg	Ala	Val	Leu	Ala	Lys	Val	Gly	Tyr	Pro	Glu
465					470					475					480
Phe	Ile	Met	Asn		Thr	His	Val		Glu	Asp	Leu	Lys	Ala	Ile	Lys
				485					490					495	
Phe	Ser	Glu	Ala	Asp	Tyr	Phe	Gly	Asn	Val	Leu	Gln	Thr	Arg	Lys	Tyr
			500					505		•			510		

WO 2005/076008 PCT/EP2005/000722

-4-

Leu Ala Gln Ser Asp Phe Phe Trp Leu Arg Lys Ala Val Pro Lys Thr 520 Glu Trp Phe Thr Asn Pro Thr Thr Val Asn Ala Phe Tyr Ser Ala Ser 535 540 Thr Asn Gln Ile Arg Phe Pro Ala Gly Glu Leu Gln Lys Pro Phe Phe 550 555 Trp Gly Thr Glu Tyr Pro Arg Ser Leu Ser Tyr Gly Ala Ile Gly Val 570 Ile Val Gly His Glu Phe Thr His Gly Phe Asp Asn Asn Gly Arg Lys 580 585 590 Tyr Asp Lys Asn Gly Asn Leu Asp Pro Trp Trp Ser Thr Glu Ser Glu 600 Glu Lys Phe Lys Glu Lys Thr Lys Cys Met Ile Asn Gln Tyr Ser Asn 615 Tyr Tyr Trp Lys Lys Ala Gly Leu Asn Val Lys Gly Lys Arg Thr Leu 630 635 Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Arg Glu Ala Phe Arg Ala 645 650 Tyr Arg Lys Trp Ile Asn Asp Arg Gln Gly Leu Glu Glu Pro Leu 665 Leu Pro Gly Ile Thr Phe Thr Asn Asn Gln Leu Phe Phe Leu Ser Tyr 680 685 Ala His Val Arg Cys Asn Ser Tyr Arg Pro Glu Ala Ala Arg Glu Gln 695 700 Val Gln Ile Gly Ala His Ser Pro Pro Gln Phe Arg Val Asn Gly Ala 710 715 Ile Ser Asn Phe Glu Glu Phe Gln Lys Ala Phe Asn Cys Pro Pro Asn 725 730 Ser Thr Met Asn Arg Gly Met Asp Ser Cys Arg Leu Trp 740 745

22

<210> 3

<211> 22

<212> DNA

<213> artificial sequence

<220>

<223> forward primer

<400> 3

tgagaaagcg attgaaaaag ca

<210> 4

<211> 16

<212> DNA

WO 2005/076008 PCT/EP2005/000722

- 5 -

<213>	artificial sequence	
<220>		
<223>	reverse primer	
<400>	4	
gggcca	gcgg aaaggt	16
<210>	5	
<211>	29	
<212>	DNA	
<213>	artificial sequence	
<220>		
<223>	probe	
<400>	5	

29

caagecactg ctacacatec tacggcatt